

SEQUENCE LISTING

<110> Han, Hui-Quan
Kwak, Keith

<120> Human E3 Alpha Ubiquitin Ligase Family

<130> 01017/35966B

<140> To be assigned

<141> Herewith

<150> US 09/724,126

<151> 2000-11-28

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<151> 1999-03-08

<160> 29

<170> PatentIn Ver. 2.0

<210> 1

<211> 6308

<212> DNA

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<221> CDS

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 Ile Tyr Cys Arg Gly Pro Asn Pro Phe Pro Gln Lys Glu Asp Met Leu
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 Ala Gln His Val Leu Leu Gly Pro Met Glu Trp Tyr Leu Cys Gly Glu
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 His Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys
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 Arg Asp Cys Ala Val Asp Pro Thr Cys Val Leu Cys Met Glu Cys Phe
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 Leu Gly Ser Ile His Arg Asp His Arg Tyr Arg Met Thr Thr Ser Gly
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 Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Glu Gly
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 Pro Tyr Cys Gln Lys His Glu Leu Asn Thr Ser Glu Ile Glu Glu Glu
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 Glu Asp Pro Leu Val His Leu Ser Glu Asp Val Ile Ala Arg Thr Tyr
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 Asn Ile Phe Ala Ile Thr Phe Arg Tyr Ala Val Glu Ile Leu Thr Trp
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1

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tat gga gag acc gac cag gga ctc aga cga gga aat cct tta cat tta Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn Pro Leu His Leu 1705 1710 1715	5913
tgc caa gag cgg ttt cga aag atc cag aag ctc tgg cag cag cat agt Cys Gln Glu Arg Phe Arg Lys Ile Gln Lys Leu Trp Gln Gln His Ser 1720 1725 1730	5961
atc aca gag gag atc gga cac gcg cag gag gct aac cag acc ctg gtc Ile Thr Glu Glu Ile Gly His Ala Gln Glu Ala Asn Gln Thr Leu Val 1735 1740 1745	6009
gga att gac tgg cag cat tta taatcgctcc tctactaaaa acttgacttg Gly Ile Asp Trp Gln His Leu 1750 1755	6060
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 <212> PRT
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 Asp Leu Asn Arg Glu Val Tyr Gln His Leu Ala His Cys Val Pro Lys
 35 40 45
 Ile Tyr Cys Arg Gly Pro Asn Pro Phe Pro Gln Lys Glu Asp Thr Leu
 50 55 60
 Ala Gln His Ile Leu Leu Gly Pro Met Glu Trp Tyr Ile Cys Ala Glu
 65 70 75 80
 Asp Pro Ala Leu Gly Phe Pro Lys Leu Glu Gln Ala Asn Lys Pro Ser
 85 90 95
 His Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys
 100 105 110
 Arg Asp Cys Ala Val Asp Pro Thr Cys Val Leu Cys Met Glu Cys Phe
 115 120 125
 Leu Gly Ser Ile His Arg Asp His Arg Tyr Arg Met Thr Thr Ser Gly
 130 135 140
 Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Glu Gly
 145 150 155 160
 Pro Tyr Cys Gln Lys His Lys Leu Ser Ser Ser Glu Val Val Glu Glu
 165 170 175
 Glu Asp Pro Leu Val His Leu Ser Glu Asp Val Ile Ala Arg Thr Tyr
 180 185 190
 Asn Ile Phe Ala Ile Met Phe Arg Tyr Ala Val Asp Ile Leu Thr Trp
 195 200 205
 Glu Lys Glu Ser Glu Leu Pro Glu Asp Leu Glu Val Ala Glu Lys Ser
 210 215 220
 Asp Thr Tyr Tyr Cys Met Leu Phe Asn Asp Glu Val His Thr Tyr Glu
 225 230 235 240
 Gln Val Ile Tyr Thr Leu Gln Lys Ala Val Asn Cys Thr Gln Lys Glu
 245 250 255
 Ala Ile Gly Phe Ala Thr Thr Val Asp Arg Asp Gly Arg Arg Pro Val
 260 265 270
 Arg Tyr Gly Asp Phe Gln Tyr Cys Asp Gln Ala Lys Thr Val Ile Val
 275 280 285
 Arg Asn Thr Ser Arg Gln Thr Lys Pro Leu Lys Val Gln Val Met His
 290 295 300

Ser Ser Val Ala Ala His Gln Asn Phe Gly Leu Lys Ala Leu Ser Trp
 305 310 315 320
 Leu Gly Ser Val Ile Gly Tyr Ser Asp Gly Leu Arg Arg Ile Leu Cys
 325 330 335
 Gln Val Gly Leu Gln Glu Gly Pro Asp Gly Glu Asn Ser Ser Leu Val
 340 345 350
 Asp Arg Leu Met Leu Asn Asp Ser Lys Leu Trp Lys Gly Ala Arg Ser
 355 360 365
 Val Tyr His Gln Leu Phe Met Ser Ser Leu Leu Met Asp Leu Lys Tyr
 370 375 380
 Lys Lys Leu Phe Ala Leu Arg Phe Ala Lys Asn Tyr Arg Gln Leu Gln
 385 390 395 400
 Arg Asp Phe Met Glu Asp Asp His Glu Arg Ala Val Ser Val Thr Ala
 405 410 415
 Leu Ser Val Gln Phe Phe Thr Ala Pro Thr Leu Ala Arg Met Leu Leu
 420 425 430
 Thr Glu Glu Asn Leu Met Thr Val Ile Ile Lys Ala Phe Met Asp His
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 Leu Lys His Arg Asp Ala Gln Gly Arg Phe Gln Phe Glu Arg Tyr Thr
 450 455 460
 Ala Leu Gln Ala Phe Lys Phe Arg Arg Val Gln Ser Leu Ile Leu Asp
 465 470 475 480
 Leu Lys Tyr Val Leu Ile Ser Lys Pro Thr Glu Trp Ser Asp Glu Leu
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 Arg Gln Lys Phe Leu Gln Gly Phe Asp Ala Phe Leu Glu Leu Leu Lys
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 Cys Met Gln Gly Met Asp Pro Ile Thr Arg Gln Val Gly Gln His Ile
 515 520 525
 Glu Met Glu Pro Glu Trp Glu Ala Ala Phe Thr Leu Gln Met Lys Leu
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 Thr His Val Ile Ser Met Val Gln Asp Trp Cys Ala Leu Asp Glu Lys
 545 550 555 560
 Val Leu Ile Glu Ala Tyr Lys Lys Cys Leu Ala Val Leu Thr Gln Cys
 565 570 575
 His Gly Gly Phe Thr Asp Gly Glu Gln Pro Ile Thr Leu Ser Ile Cys
 580 585 590
 Gly His Ser Val Glu Thr Ile Arg Tyr Cys Val Ser Gln Glu Lys Val
 595 600 605
 Ser Ile His Leu Pro Ile Ser Arg Leu Leu Ala Gly Leu His Val Leu
 610 615 620
 Leu Ser Lys Ser Glu Val Ala Tyr Lys Phe Pro Glu Leu Leu Pro Leu
 625 630 635 640

Ser Glu Leu Ser Pro Pro Met Leu Ile Glu His Pro Leu Arg Cys Leu
 645 650 655
 Val Leu Cys Ala Gln Val His Ala Gly Met Trp Arg Arg Asn Gly Phe
 660 665 670
 Ser Leu Val Asn Gln Ile Tyr Tyr Tyr His Asn Val Lys Cys Arg Arg
 675 680 685
 Glu Met Phe Asp Lys Asp Ile Val Met Leu Gln Thr Gly Val Ser Met
 690 695 700
 Met Asp Pro Asn His Phe Leu Met Ile Met Leu Ser Arg Phe Glu Leu
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 Tyr Gln Leu Phe Ser Thr Pro Asp Tyr Gly Lys Arg Phe Ser Ser Glu
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 Val Thr His Lys Asp Val Val Gln Gln Asn Asn Thr Leu Ile Glu Glu
 740 745 750
 Met Leu Tyr Leu Ile Ile Met Leu Val Gly Glu Arg Phe Asn Pro Gly
 755 760 765
 Val Gly Gln Val Ala Ala Thr Asp Glu Ile Lys Arg Glu Ile Ile His
 770 775 780
 Gln Leu Ser Ile Lys Pro Met Ala His Ser Glu Leu Val Lys Ser Leu
 785 790 795 800
 Pro Glu Asp Glu Asn Lys Glu Thr Gly Met Glu Ser Val Ile Glu Ser
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 Val Ala His Phe Lys Lys Pro Gly Leu Thr Gly Arg Gly Met Tyr Glu
 820 825 830
 Leu Lys Pro Glu Cys Ala Lys Glu Phe Asn Leu Tyr Phe Tyr His Phe
 835 840 845
 Ser Arg Ala Glu Gln Ser Lys Ala Glu Glu Ala Gln Arg Lys Leu Lys
 850 855 860
 Arg Glu Asn Lys Glu Asp Thr Ala Leu Pro Pro Pro Ala Leu Pro Pro
 865 870 875 880
 Phe Cys Pro Leu Phe Ala Ser Leu Val Asn Ile Leu Gln Cys Asp Val
 885 890 895
 Met Leu Tyr Ile Met Gly Thr Ile Leu Gln Trp Ala Val Glu His His
 900 905 910
 Gly Ser Ala Trp Ser Glu Ser Met Leu Gln Arg Val Leu His Leu Ile
 915 920 925
 Gly Met Ala Leu Gln Glu Glu Lys His His Leu Glu Asn Ala Val Glu
 930 935 940
 Gly His Val Gln Thr Phe Thr Phe Thr Gln Lys Ile Ser Lys Pro Gly
 945 950 955 960
 Asp Ala Pro His Asn Ser Pro Ser Ile Leu Ala Met Leu Glu Thr Leu
 965 970 975

Gln Asn Ala Pro Ser Leu Glu Ala His Lys Asp Met Ile Arg Trp Leu
 980 985 990
 Leu Lys Met Phe Asn Ala Ile Lys Lys Ile Arg Glu Cys Ser Ser Ser
 995 1000 1005
 Ser Pro Val Ala Glu Ala Glu Gly Thr Ile Met Glu Glu Ser Ser Arg
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 Asp Lys Asp Lys Ala Glu Arg Lys Arg Lys Ala Glu Ile Ala Arg Leu
 025 1030 1035 1040
 Arg Arg Glu Lys Ile Met Ala Gln Met Ser Glu Met Gln Arg His Phe
 1045 1050 1055
 Ile Asp Glu Asn Lys Glu Leu Phe Gln Gln Thr Leu Glu Leu Asp Thr
 1060 1065 1070
 Ser Ala Ser Ala Thr Leu Asp Ser Ser Pro Pro Val Ser Asp Ala Ala
 1075 1080 1085
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 1090 1095 1100
 Phe Val Thr Cys Ile Leu Cys Gln Glu Glu Gln Glu Val Thr Val Gly
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 Ser Arg Ala Met Val Leu Ala Ala Phe Val Gln Arg Ser Thr Val Leu
 1125 1130 1135
 Ser Lys Asp Arg Thr Lys Thr Ile Ala Asp Pro Glu Lys Tyr Asp Pro
 1140 1145 1150
 Leu Phe Met His Pro Asp Leu Ser Cys Gly Thr His Thr Gly Ser Cys
 1155 1160 1165
 Gly His Val Met His Ala His Cys Trp Gln Arg Tyr Phe Asp Ser Val
 1170 1175 1180
 Gln Ala Lys Glu Gln Arg Arg Gln Gln Arg Leu Arg Leu His Thr Ser
 185 1190 1195 1200
 Tyr Asp Val Glu Asn Gly Glu Phe Leu Cys Pro Leu Cys Glu Cys Leu
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 Ser Asn Thr Val Ile Pro Leu Leu Leu Pro Pro Arg Ser Ile Leu Ser
 1220 1225 1230
 Arg Arg Leu Asn Phe Ser Asp Gln Pro Asp Leu Ala Gln Trp Thr Arg
 1235 1240 1245
 Ala Val Thr Gln Gln Ile Lys Val Val Gln Met Leu Arg Arg Lys His
 1250 1255 1260
 Asn Ala Ala Asp Thr Ser Ser Ser Glu Asp Thr Glu Ala Met Asn Ile
 265 1270 1275 1280
 Ile Pro Ile Pro Glu Gly Phe Arg Pro Asp Phe Tyr Pro Arg Asn Pro
 1285 1290 1295
 Tyr Ser Asp Ser Ile Lys Glu Met Leu Thr Thr Phe Gly Thr Ala Ala
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Tyr Lys Val Gly Leu Lys Val His Pro Asn Glu Gly Asp Pro Arg Val
 1315 1320 1325
 Pro Ile Leu Cys Trp Gly Thr Cys Ala Tyr Thr Ile Gln Ser Ile Glu
 1330 1335 1340
 Arg Ile Leu Ser Asp Glu Glu Lys Pro Val Phe Gly Pro Leu Pro Cys
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 Arg Leu Asp Asp Cys Leu Arg Ser Leu Thr Arg Phe Ala Ala Ala His
 1365 1370 1375
 Trp Thr Val Ala Leu Leu Pro Val Val Gln Gly His Phe Cys Lys Leu
 1380 1385 1390
 Phe Ala Ser Leu Val Pro Ser Asp Ser Tyr Glu Asp Leu Pro Cys Ile
 1395 1400 1405
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 Pro Ala Leu Gln Cys Gln Asp Phe Ser Gly Ser Ser Leu Ala Thr Gly
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 Asp Leu His Ile Phe His Leu Val Thr Met Ala His Ile Val Gln Ile
 1445 1450 1455
 Leu Leu Thr Ser Cys Thr Glu Glu Asn Gly Met Asp Gln Glu Asn Pro
 1460 1465 1470
 Thr Gly Glu Glu Glu Leu Ala Ile Leu Ser Leu His Lys Thr Leu His
 1475 1480 1485
 Gln Tyr Thr Gly Ser Ala Leu Lys Glu Ala Pro Ser Gly Trp His Leu
 1490 1495 1500
 Trp Arg Ser Val Arg Ala Ala Ile Met Pro Phe Leu Lys Cys Ser Ala
 505 1510 1515 1520
 Leu Phe Phe His Tyr Leu Asn Gly Val Pro Ala Pro Pro Asp Leu Gln
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 Val Ser Gly Thr Ser His Phe Glu His Leu Cys Asn Tyr Leu Ser Leu
 1540 1545 1550
 Pro Thr Asn Leu Ile His Leu Phe Gln Glu Asn Ser Asp Ile Met Asn
 1555 1560 1565
 Ser Leu Ile Glu Ser Trp Cys Gln Asn Ser Glu Val Lys Arg Tyr Leu
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 Asn Gly Glu Arg Gly Ala Ile Ser Tyr Pro Arg Gly Ala Asn Lys Leu
 585 1590 1595 1600
 Ile Asp Leu Pro Glu Asp Tyr Ser Ser Leu Ile Asn Gln Ala Ser Asn
 1605 1610 1615
 Phe Ser Cys Pro Lys Ser Gly Gly Asp Lys Ser Arg Ala Pro Thr Leu
 1620 1625 1630
 Cys Leu Val Cys Gly Ser Leu Leu Cys Ser Gln Ser Tyr Cys Cys Gln
 1635 1640 1645

Ala Glu Leu Glu Gly Glu Asp Val Gly Ala Cys Thr Ala His Thr Tyr
1650 1655 1660

Ser Cys Gly Ser Gly Ala Gly Ile Phe Leu Arg Val Arg Glu Cys Gln
665 1670 1675 1680

Val Leu Phe Leu Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro
1685 1690 1695

Tyr Leu Asp Asp Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn
1700 1705 1710

Pro Leu His Leu Cys Gln Glu Arg Phe Arg Lys Ile Gln Lys Leu Trp
1715 1720 1725

Gln Gln His Ser Ile Thr Glu Glu Ile Gly His Ala Gln Glu Ala Asn
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Gln Thr Leu Val Gly Ile Asp Trp Gln His Leu
745 1750 1755

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<213> Artificial Sequence

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-2282-91

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21

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<212> DNA
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<220>
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2385-35

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24

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<213> Artificial Sequence

<220>
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23

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer 2294-37

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23

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<211> 18

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer 2380-88

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18

<210> 12

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2378-32

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23

<210> 13

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer 2381-48

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23

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer 2385-94

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<212> PRT

<213> Mouse

<400> 15

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Glu	Pro	Pro	Leu	Ala	Pro	Gln	Arg	Pro	Ala	Ser	Trp	Trp	Asp	Gln	Gln	20	25	30	
Val	Asp	Phe	Tyr	Thr	Ala	Phe	Leu	His	His	Leu	Ala	Gln	Leu	Val	Pro	35	40	45	
Glu	Ile	Tyr	Phe	Ala	Glu	Met	Asp	Pro	Asp	Leu	Glu	Lys	Gln	Glu	Glu	50	55	60	
Ser	Val	Gln	Met	Ser	Ile	Leu	Thr	Pro	Leu	Glu	Trp	Tyr	Leu	Phe	Gly	65	70	75	80
Glu	Asp	Pro	Asp	Ile	Cys	Leu	Glu	Lys	Leu	Lys	His	Ser	Gly	Ala	Phe	85	90	95	
Gln	Leu	Cys	Gly	Lys	Val	Phe	Lys	Ser	Gly	Glu	Thr	Thr	Tyr	Ser	Cys	100	105	110	
Arg	Asp	Cys	Ala	Ile	Asp	Pro	Thr	Cys	Val	Leu	Cys	Met	Asp	Cys	Phe	115	120	125	
Gln	Ser	Ser	Val	His	Lys	Asn	His	Arg	Tyr	Lys	Met	His	Thr	Ser	Thr	130	135	140	
Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Thr	Gly	145	150	155	160
Pro	Phe	Cys	Val	Asp	His	Glu	Pro	Gly	Arg	Ala	Gly	Thr	Thr	Lys	Glu	165	170	175	
Ser	Leu	His	Cys	Pro	Leu	Asn	Glu	Glu	Val	Ile	Ala	Gln	Ala	Arg	Arg	180	185	190	
Ile	Phe	Pro	Ser	Val	Ile	Lys	Tyr	Ile	Val	Glu	Met	Thr	Ile	Trp	Glu	195	200	205	
Glu	Glu	Lys	Glu	Leu	Pro	Pro	Glu	Leu	Gln	Ile	Arg	Glu	Lys	Asn	Glu	210	215	220	
Arg	Tyr	Tyr	Cys	Val	Leu	Phe	Asn	Asp	Glu	His	His	Ser	Tyr	Asp	His	225	230	235	240
Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys	Glu	Leu	Ala	Glu	Ala	245	250	255	
Gln	Leu	His	Thr	Thr	Ala	Ile	Asp	Lys	Glu	Gly	Arg	Arg	Ala	Val	Lys	260	265	270	
Ala	Gly	Val	Tyr	Ala	Thr	Cys	Gln	Glu	Ala	Lys	Glu	Asp	Ile	Lys	Ser	275	280	285	
His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His	Val	Glu	Val	Leu	His	290	295	300	
Ser	Val	Val	Met	Ala	His	Gln	Lys	Phe	Ala	Leu	Arg	Leu	Gly	Ser	Trp	305	310	315	320
Met	Asn	Lys	Ile	Met	Ser	Tyr	Ser	Ser	Asp	Phe	Arg	Gln	Ile	Phe	Cys	325	330	335	

Gln	Ala	Cys	Leu	Val	Glu	Glu	Pro	Gly	Ser	Glu	Asn	Pro	Cys	Leu	Ile	
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Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr	Lys	Gly	Ala	Arg	Lys	
		355					360					365				
Ile	Leu	His	Glu	Leu	Ile	Phe	Ser	Ser	Phe	Phe	Met	Glu	Met	Glu	Tyr	
	370					375					380					
Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr	Tyr	Lys	Gln	Leu	Gln	
385					390					395					400	
Lys	Glu	Tyr	Ile	Ser	Asp	Asp	His	Glu	Arg	Ser	Ile	Ser	Ile	Thr	Ala	
				405					410					415		
Leu	Ser	Val	Gln	Met	Leu	Thr	Val	Pro	Thr	Leu	Ala	Arg	His	Leu	Ile	
			420					425					430			
Glu	Glu	Gln	Asn	Val	Ile	Ser	Val	Ile	Thr	Glu	Thr	Leu	Leu	Glu	Val	
		435					440					445				
Leu	Pro	Glu	Tyr	Leu	Asp	Arg	Asn	Asn	Lys	Phe	Asn	Phe	Gln	Gly	Tyr	
	450					455					460					
Ser	Gln	Asp	Lys	Leu	Gly	Arg	Val	Tyr	Ala	Val	Ile	Cys	Asp	Leu	Lys	
465					470					475					480	
Tyr	Ile	Leu	Ile	Ser	Lys	Pro	Val	Ile	Trp	Thr	Glu	Arg	Leu	Arg	Ala	
				485					490					495		
Gln	Phe	Leu	Glu	Gly	Phe	Arg	Ser	Phe	Leu	Lys	Ile	Leu	Thr	Cys	Met	
		500						505					510			
Gln	Gly	Met	Glu	Glu	Ile	Arg	Arg	Gln	Val	Gly	Gln	His	Ile	Glu	Val	
		515					520					525				
Asp	Pro	Asp	Trp	Glu	Ala	Ala	Ile	Ala	Ile	Gln	Met	Gln	Leu	Lys	Asn	
	530					535					540					
Ile	Leu	Leu	Met	Phe	Gln	Glu	Trp	Cys	Ala	Cys	Asp	Glu	Asp	Leu	Leu	
545					550					555					560	
Leu	Val	Ala	Tyr	Lys	Glu	Cys	His	Lys	Ala	Val	Met	Arg	Cys	Ser	Thr	
				565					570					575		
Asn	Phe	Met	Ser	Ser	Thr	Lys	Thr	Val	Val	Gln	Leu	Cys	Gly	His	Ser	
			580					585					590			
Leu	Glu	Thr	Lys	Ser	Tyr	Lys	Val	Ser	Glu	Asp	Leu	Val	Ser	Ile	His	
		595					600					605				
Leu	Pro	Leu	Ser	Arg	Thr	Leu	Ala	Gly	Leu	His	Val	Arg	Leu	Ser	Arg	
	610					615					620					
Leu	Gly	Ala	Ile	Ser	Arg	Leu	His	Glu	Phe	Val	Pro	Phe	Asp	Ser	Phe	
625					630					635					640	
Gln	Val	Glu	Val	Leu	Val	Glu	Tyr	Pro	Leu	Arg	Cys	Leu	Val	Leu	Val	
				645					650					655		
Ala	Gln	Val	Val	Ala	Glu	Met	Trp	Arg	Arg	Asn	Gly	Leu	Ser	Leu	Ile	
			660					665					670			

Ser Gln Val Phe Tyr Tyr Gln Asp Val Lys Cys Arg Glu Glu Met Tyr
 675 680 685
 Asp Lys Asp Ile Ile Met Leu Gln Ile Gly Ala Ser Ile Met Asp Pro
 690 695 700
 Asn Lys Phe Leu Leu Leu Val Leu Gln Arg Tyr Glu Leu Thr Asp Ala
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 Phe Asn Lys Thr Ile Ser Thr Lys Asp Gln Asp Leu Ile Lys Gln Tyr
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 Asn Thr Leu Ile Glu Glu Met Leu Gln Val Leu Ile Tyr Ile Val Gly
 740 745 750
 Glu Arg Tyr Val Pro Gly Val Gly Asn Val Thr Arg Glu Glu Val Ile
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 Met Arg Glu Ile Thr His Leu Leu Cys Ile Glu Pro Met Pro His Ser
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 Ala Ile Ala Arg Asn Leu Pro Glu Asn Glu Asn Asn Glu Thr Gly Leu
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 Glu Asn Val Ile Asn Lys Val Ala Thr Phe Lys Lys Pro Gly Val Ser
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 Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser Leu Lys Asp Phe Asn
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 Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His Ser Lys Ala Glu His
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 Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys Asp Glu Ala Leu Pro
 850 855 860
 Pro Pro Pro Pro Pro Glu Phe Cys Pro Ala Phe Ser Lys Val Val Asn
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 Arg Ala Val Asp Thr Glu Ser Asn Leu Trp Thr Glu Gly Met Leu Gln
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 Met Ala Phe His Ile Leu Ala Leu Gly Leu Leu Glu Glu Lys Gln Gln
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 Leu Gln Lys Ala Pro Glu Glu Glu Val Ala Phe Asp Phe Tyr His Lys
 930 935 940
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 965 970 975
 Met Ile Thr Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg Leu Arg
 980 985 990
 Glu Lys Ser Cys Leu Val Val Ala Thr Thr Ser Gly Leu Glu Cys Ile
 995 1000 1005

Lys Ser Glu Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg Lys Arg
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 Lys Ala Glu Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala Gln Met
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 Ser Ala Leu Gln Lys Asn Phe Ile Glu Thr His Lys Leu Met Tyr Asp
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 Asn Thr Ser Glu Val Thr Gly Lys Glu Asp Ser Ile Met Glu Glu Glu
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 Ser Thr Ser Ala Val Ser Glu Ala Ser Arg Ile Ala Leu Gly Pro Lys
 1075 1080 1085
 Arg Gly Pro Ala Val Thr Glu Lys Glu Val Leu Thr Cys Ile Leu Cys
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 Gln Glu Glu Gln Glu Val Lys Leu Glu Asn Asn Ala Met Val Leu Ser
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 Ala Cys Val Gln Lys Ser Thr Ala Leu Thr Gln His Arg Gly Lys Pro
 1125 1130 1135
 Val Asp His Leu Gly Glu Thr Leu Asp Pro Leu Phe Met Asp Pro Asp
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 Leu Ala His Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met His Ala
 1155 1160 1165
 Val Cys Trp Gln Lys Tyr Phe Glu Ala Val Gln Leu Ser Ser Gln Gln
 1170 1175 1180
 Arg Ile His Val Asp Leu Phe Asp Leu Glu Ser Gly Glu Tyr Leu Cys
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 Pro Leu Cys Lys Ser Leu Cys Asn Thr Val Ile Pro Ile Ile Pro Leu
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 Gln Pro Gln Lys Ile Asn Ser Glu Asn Ala Glu Ala Leu Ala Gln Leu
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 Leu Thr Leu Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile Ser Gly
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 Tyr Asn Ile Lys His Ala Lys Gly Glu Ala Pro Ala Val Pro Val Leu
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 Phe Asn Gln Gly Met Gly Asp Ser Thr Phe Glu Phe His Ser Ile Leu
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 Ser Phe Gly Val Gln Ser Ser Val Lys Tyr Ser Asn Ser Ile Lys Glu
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 Met Val Ile Leu Phe Ala Thr Thr Ile Tyr Arg Ile Gly Leu Lys Val
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 Pro Pro Asp Glu Leu Asp Pro Arg Val Pro Met Met Thr Trp Ser Thr
 1315 1320 1325
 Cys Ala Phe Thr Ile Gln Ala Ile Glu Asn Leu Leu Gly Asp Glu Gly
 1330 1335 1340

Lys Pro Leu Phe Gly Ala Leu Gln Asn Arg Gln His Ser Gly Leu Lys
 1345 1350 1355 1360
 Ala Leu Met Gln Phe Ala Val Ala Gln Arg Ala Thr Cys Pro Gln Val
 1365 1370 1375
 Leu Ile His Lys His Leu Ala Arg Leu Leu Ser Val Ile Leu Pro Asn
 1380 1385 1390
 Leu Gln Ser Glu Asn Thr Pro Gly Leu Leu Ser Val Asp Leu Phe His
 1395 1400 1405
 Val Leu Val Gly Ala Val Leu Ala Phe Pro Ser Leu Tyr Trp Asp Asp
 1410 1415 1420
 Thr Val Asp Leu Gln Pro Ser Pro Leu Ser Ser Ser Tyr Asn His Leu
 1425 1430 1435 1440
 Tyr Leu Phe His Leu Ile Thr Met Ala His Met Leu Gln Ile Leu Leu
 1445 1450 1455
 Thr Thr Asp Thr Asp Leu Ser Pro Gly Pro Pro Leu Ala Glu Gly Glu
 1460 1465 1470
 Glu Asp Ser Glu Glu Ala Arg Cys Ala Ser Ala Phe Phe Val Glu Val
 1475 1480 1485
 Ser Gln His Thr Asp Gly Leu Thr Gly Cys Gly Ala Pro Gly Trp Tyr
 1490 1495 1500
 Leu Trp Leu Ser Leu Arg Asn Gly Ile Thr Pro Tyr Leu Arg Cys Ala
 1505 1510 1515 1520
 Ala Leu Leu Phe His Tyr Leu Leu Gly Val Ala Pro Pro Glu Glu Leu
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 Phe Ala Asn Ser Ala Glu Gly Glu Phe Ser Ala Leu Cys Ser Tyr Leu
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 Ser Leu Pro Thr Asn Leu Phe Leu Leu Phe Gln Glu Tyr Trp Asp Thr
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 Ile Arg Pro Leu Leu Gln Arg Trp Cys Gly Asp Pro Ala Leu Leu Lys
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 Ser Leu Lys Gln Lys Ser Ala Val Val Arg Tyr Pro Arg Lys Arg Asn
 1585 1590 1595 1600
 Ser Leu Ile Glu Leu Pro Glu Asp Tyr Ser Cys Leu Leu Asn Gln Ala
 1605 1610 1615
 Ser His Phe Arg Cys Pro Arg Ser Ala Asp Asp Glu Arg Lys His Pro
 1620 1625 1630
 Val Leu Cys Leu Phe Cys Gly Ala Ile Leu Cys Ser Gln Asn Ile Cys
 1635 1640 1645
 Cys Gln Glu Ile Val Asn Gly Glu Glu Val Gly Ala Cys Val Phe His
 1650 1655 1660
 Ala Leu His Cys Gly Ala Gly Val Cys Ile Phe Leu Lys Ile Arg Glu
 1665 1670 1675 1680

Cys Arg Val Val Leu Val Glu Gly Lys Ala Arg Gly Cys Ala Tyr Pro
1685 1690 1695

Ala Pro Tyr Leu Asp Glu Tyr Gly Glu Thr Asp Pro Gly Leu Lys Arg
1700 1705 1710

Gly Asn Pro Leu His Leu Ser Arg Glu Arg Tyr Arg Lys Leu His Leu
1715 1720 1725

Val Trp Gln Gln His Cys Ile Ile Glu Glu Ile Ala Arg Ser Gln Glu
1730 1735 1740

Thr Asn Gln Met Leu Phe Gly Phe Asn Trp Gln Leu Leu
1745 1750 1755

<210> 16
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 16
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 17
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 17
Gly Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10 15

<210> 18
<211> 5205
<212> DNA
<213> Homo sapiens

<400> 18
atggcgagc agggagctgg aggtactgag aggatggaaa tcagcgcgga gttacccag 60
accctcagc gtctggcatc ttggtgggat cagcaagttg atttttatac tgctttcttg 120
catcatttg cacaattggt gccagaaatt tactttgctg aaatggaccc agacttgga 180
aagcaggagg aaagtgtaca aatgtcaata ttcactccac tggaatggta cttatttgga 240
gaagatccag atatttgctt agagaaattg aagcacagtg gagcatttca gctttgtggg 300
agggttttca aaagtggaga gacaacctat tcttgcaggg attgtgcaat tgatccaaca 360
tgtgtactct gtatggactg cttccaggac agtgttcata aaaatcatcg ttacaagatg 420
catacttcta ctggaggagg gttctgtgac tgtggagaca cagaggcatg gaaaactggc 480

cctttttgtg taaatcatga acctggaaga gcaggtacta taaaagagaa ttcacgctgt 540
ccgttgaatg aagaggtaat tgtccaagcc aggaaaatat ttccttcagt gataaaatat 600
gtcgtagaaa tgactatatg ggaagaggaa aaagaactgc ctctgaact ccagataagg 660
knryycvndh hsydhgtcat atacagccta caaagagctc ttgactgtga gctcgcagag 720
gcccagttgc ataccactgc cattgacaaa gagggtcgtc gggctgttaa agcgggagct 780
tatgctgctt gccaggaagc aaaggaagat ataaagagtc attcagaaaa tgtctctcaa 840
catccacttc atgtagaagt attacactca gagattatgg ctcatcagaa atttgctttg 900
cgtcttggtt cctggatgaa caaaattatg agctattcaa gtgactttag gcagatcttt 960
tgccaagcat gccttagaga agaacctgac tcggagaatc cctgtctcat aagcaggtta 1020
atgctttggg atgcaaagct ttataaaggt gcccgtaaga tccttcatga attgatcttc 1080
agcagttttt ttatggagat ggaatacaaa aaactctttg ctatggaatt tgtgaagtat 1140
tataaacaac tgcagaaaga atatatcagt gatgatcatg acagaagtat ctctataact 1200
gcactttcag ttcagatggt tactgttcct actctggctc gacatcttat tgaagagcag 1260
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aacaataaat tcaacttcca gggttatagc caggacaaat tgggaagagt atatgcagta 1380
atatgtgacc taaagtatat cctgatcagc aaaccacaa tatggacaga aagattaaga 1440
atgcagttcc ttgaagggtt tcgatctttt ttgaagattc ttacctgtat gcagggaatg 1500
gaagaaatcc gaagacagg tgggcaacac attgaagtgg atcctgattg ggaggctgcc 1560
attgctatac agatgcaatt gaagaatatt ttactcatgt tccaagagtg gtgtgcttgt 1620
gatgaagaac tcttacttgt ggcttataaa gaatgtcaca aagctgtgat gaggtgcagt 1680
accagtttca tatctagtag caagacagta gtacaatcgt gtggacatag tttggaaaca 1740
aagtcctaca gagtatctga ggatcttgta agcatacatc tgccactctc taggaccctt 1800
gctggctctc atgtacgttt aagcaggctg ggtgctgttt caagactgca tgaatttgtg 1860
tcttttgagg actttcaagt agaggacta gtggaatatc ctttacgttg tctgggtgtg 1920
gttgccagg ttgttgctga gatgtggcga agaaatggac tgtctcttat tagccagggtg 1980
ttttattacc aagatgttaa gtgcagagaa gaaatgtatg ataaagatat catcatgctt 2040
cagattggtg catctttaat ggatcccaat aagttcttgt tactgggtact tcagagggtat 2100
gaacttgccg aggcttttaa caagaccata tctacaaaag accaggattt gattaaacaa 2160
tataatacac taatagaaga aatgcttcag gtcctcatct atattgtggg tgagcgttat 2220
gtacctggag tgggaaatgt gaccaaagaa gaggtcacia tgagagaaat cattcacttg 2280
ctttgcattg aacccatgcc acacagtgcc attgccaaaa atttacctga gaatgaaaat 2340
aatgaaactg gcttagagaa tgtcataaac aaagtggcca catttaagaa accagggtgta 2400

tcaggccatg gagtttatga actaaaagat gaatcactga aagacttcaa tatgtacttt 2460
 tatcattact ccaaaaccca gcatagcaag gctgaacata tgcagaagaa aaggagaaaa 2520
 caagaaaaca aagatgaagc attgccgcca ccaccacctc ctgaattctg ccctgctttc 2580
 agcaaagtga ttaaccttct caactgtgat atcatgatgt acattctcag gaccgtattt 2640
 gagcgggcaa tagacacaga ttctaacttg tggaccgaag ggatgctcca aatggctttt 2700
 catattctgg cattgggttt actagaagag aagcaacagc ttcaaaaagc tcctgaagaa 2760
 gaagtaacat ttgactttta tcataaggct tcaagattgg gaagttcagc catgaatata 2820
 caaatgcttt tggaaaaact caaaggaatt ccccgattag aaggccagaa ggacatgata 2880
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 gtagcaacca catcaggatc ggaatctatt aagaatgatg agattactca tgataaagaa 3000
 aaagcagaac gaaaaagaaa agctgaagct gctaggctac atcgccagaa gatcatggct 3060
 cagatgtctg ccttacagaa aaacttcatt gaaactcata aactcatgta tgacaatata 3120
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 gactactcta gaattgcttt gggtcctaaa cgggtccat ctgttactga aaaggaggtg 3240
 ctgacgtgca tcctttgcca agaagaacag gaggtgaaaa tagaaaataa tgccatggta 3300
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 ctctcaggag aagccctaga cccacttttc atggatccag acttggcata tggaacttat 3420
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 ctttgccctc tttgcaaate tctgtgcaat actgtgatcc ccattattcc tttgcaacct 3600
 caaaagataa acagtgagaa tgcagatgct cttgctcaac ttttgaccct ggcacgggtg 3660
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 ccaattccta ttttctttta tcaaggaatg ggagattcta ctttggagtt ccattccatc 3780
 ctgagttttg gcgttgagtc ttcgattaaa tattcaaata gcatcaagga aatggttatt 3840
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 ttgtattggg atgacctgt tgatctgcag ccttcttcag ttagttcttc ctataaccac 4260
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 gaatattggg atactgtaag gcccttgctc cagaggcggt gtgcagatcc tgccttacta 4680
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 tctgcagatg atgagcgaaa gcatcctgct ctctgccttt tctgtggggc tatactatgt 4860
 tctcagaaca tttgctgccca ggaaattgtg aacggggaag aggttgaggc ttgcattttt 4920
 cacgcacttc actgtggagc cggagtctgc attttcctaa aaatcagaga atgccgagtg 4980
 gtcctgggtg aaggtaaagc cagaggctgt gcctatccag ctccttactt ggatgaatat 5040
 ggagaaacag accctggcct gaagaggggc aacccccctt atttatctcg tgagcgggat 5100
 cggaagctcc atttggtctg gcaacaacac tgcattatag aagagattgc taggagccaa 5160
 gagactaatc agatgttatt tggattcaac tggcagttac tgtga 5205

<210> 19
 <211> 1735
 <212> PRT
 <213> Homo sapiens

<400> 19
 Ala Met Glu Gly Asn Met Ala Asp Glu Glu Ala Gly Gly Thr Glu Arg
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 Met Glu Ile Ser Ala Glu Leu Pro Gln Thr Pro Gln Arg Leu Ala Ser
 20 25 30
 Trp Trp Asp Gln Gln Val Asp Phe Tyr Thr Ala Phe Leu His His Leu
 35 40 45
 Ala Gln Leu Val Pro Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu
 50 55 60
 Glu Lys Gln Glu Glu Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu
 65 70 75 80
 Trp Tyr Leu Phe Gly Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys
 85 90 95
 His Ser Gly Ala Phe Gln Leu Cys Gly Arg Val Phe Lys Ser Gly Glu
 100 105 110
 Thr Thr Tyr Ser Cys Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu
 115 120 125
 Cys Met Asp Cys Phe Gln Asp Ser Val His Lys Asn His Arg Tyr Lys
 130 135 140

Met	His	Thr	Ser	Thr	Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	145	150	155	160
Ala	Trp	Lys	Thr	Gly	Pro	Phe	Cys	Val	Asn	His	Glu	Pro	Gly	Arg	Ala	165	170	175	
Gly	Thr	Ile	Lys	Glu	Asn	Ser	Arg	Cys	Pro	Leu	Asn	Glu	Glu	Val	Ile	180	185	190	
Val	Gln	Ala	Arg	Lys	Ile	Phe	Pro	Ser	Val	Ile	Lys	Tyr	Val	Val	Glu	195	200	205	
Met	Thr	Ile	Trp	Glu	Glu	Glu	Lys	Glu	Leu	Pro	Pro	Glu	Leu	Gln	Ile	210	215	220	
Arg	Glu	Lys	Asn	Glu	Arg	Tyr	Tyr	Cys	Val	Leu	Phe	Asn	Asp	Glu	His	225	230	235	240
His	Ser	Tyr	Asp	His	Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys	245	250	255	
Glu	Leu	Ala	Glu	Ala	Gln	Leu	His	Thr	Thr	Ala	Ile	Asp	Lys	Glu	Gly	260	265	270	
Arg	Arg	Ala	Val	Lys	Ala	Gly	Ala	Tyr	Ala	Ala	Cys	Gln	Glu	Ala	Lys	275	280	285	
Glu	Asp	Ile	Lys	Ser	His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His	290	295	300	
Val	Glu	Val	Leu	His	Ser	Glu	Ile	Met	Ala	His	Gln	Lys	Phe	Ala	Leu	305	310	315	320
Arg	Leu	Gly	Ser	Trp	Met	Asn	Lys	Ile	Met	Ser	Tyr	Ser	Ser	Asp	Phe	325	330	335	
Arg	Gln	Ile	Phe	Cys	Gln	Ala	Cys	Leu	Arg	Glu	Glu	Pro	Asp	Ser	Glu	340	345	350	
Asn	Pro	Cys	Leu	Ile	Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr	355	360	365	
Lys	Gly	Ala	Arg	Lys	Ile	Leu	His	Glu	Leu	Ile	Phe	Ser	Ser	Phe	Phe	370	375	380	
Met	Glu	Met	Glu	Tyr	Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr	385	390	395	400
Tyr	Lys	Gln	Leu	Gln	Lys	Glu	Tyr	Ile	Ser	Asp	Asp	His	Asp	Arg	Ser	405	410	415	
Ile	Ser	Ile	Thr	Ala	Leu	Ser	Val	Gln	Met	Phe	Thr	Val	Pro	Thr	Leu	420	425	430	
Ala	Arg	His	Leu	Ile	Glu	Glu	Gln	Asn	Val	Ile	Ser	Val	Ile	Thr	Glu	435	440	445	
Thr	Leu	Leu	Glu	Val	Leu	Pro	Glu	Tyr	Leu	Asp	Arg	Asn	Asn	Lys	Phe	450	455	460	
Asn	Phe	Gln	Gly	Tyr	Ser	Gln	Asp	Lys	Leu	Gly	Arg	Val	Tyr	Ala	Val	465	470	475	480

Ile	Cys	Asp	Leu	Lys	Tyr	Ile	Leu	Ile	Ser	Lys	Pro	Thr	Ile	Trp	Thr	
				485					490					495		
Glu	Arg	Leu	Arg	Met	Gln	Phe	Leu	Glu	Gly	Phe	Arg	Ser	Phe	Leu	Lys	
			500					505					510			
Ile	Leu	Thr	Cys	Met	Gln	Gly	Met	Glu	Glu	Ile	Arg	Arg	Gln	Val	Gly	
		515					520					525				
Gln	His	Ile	Glu	Val	Asp	Pro	Asp	Trp	Glu	Ala	Ala	Ile	Ala	Ile	Gln	
	530					535					540					
Met	Gln	Leu	Lys	Asn	Ile	Leu	Leu	Met	Phe	Gln	Glu	Trp	Cys	Ala	Cys	
545				550						555					560	
Asp	Glu	Glu	Leu	Leu	Leu	Val	Ala	Tyr	Lys	Glu	Cys	His	Lys	Ala	Val	
			565						570					575		
Met	Arg	Cys	Ser	Thr	Ser	Phe	Ile	Ser	Ser	Ser	Lys	Thr	Val	Val	Gln	
			580					585					590			
Ser	Cys	Gly	His	Ser	Leu	Glu	Thr	Lys	Ser	Tyr	Arg	Val	Ser	Glu	Asp	
		595					600					605				
Leu	Val	Ser	Ile	His	Leu	Pro	Leu	Ser	Arg	Thr	Leu	Ala	Gly	Leu	His	
	610					615					620					
Val	Arg	Leu	Ser	Arg	Leu	Gly	Ala	Val	Ser	Arg	Leu	His	Glu	Phe	Val	
625					630					635					640	
Ser	Phe	Glu	Asp	Phe	Gln	Val	Glu	Val	Leu	Val	Glu	Tyr	Pro	Leu	Arg	
			645						650					655		
Cys	Leu	Val	Leu	Val	Ala	Gln	Val	Val	Ala	Glu	Met	Trp	Arg	Arg	Asn	
		660						665					670			
Gly	Leu	Ser	Leu	Ile	Ser	Gln	Val	Phe	Tyr	Tyr	Gln	Asp	Val	Lys	Cys	
		675					680					685				
Arg	Glu	Glu	Met	Tyr	Asp	Lys	Asp	Ile	Ile	Met	Leu	Gln	Ile	Gly	Ala	
	690					695					700					
Ser	Leu	Met	Asp	Pro	Asn	Lys	Phe	Leu	Leu	Leu	Val	Leu	Gln	Arg	Tyr	
705					710					715					720	
Glu	Leu	Ala	Glu	Ala	Phe	Asn	Lys	Thr	Ile	Ser	Thr	Lys	Asp	Gln	Asp	
			725						730					735		
Leu	Ile	Lys	Gln	Tyr	Asn	Thr	Leu	Ile	Glu	Glu	Met	Leu	Gln	Val	Leu	
		740						745					750			
Ile	Tyr	Ile	Val	Gly	Glu	Arg	Tyr	Val	Pro	Gly	Val	Gly	Asn	Val	Thr	
	755						760					765				
Lys	Glu	Glu	Val	Thr	Met	Arg	Glu	Ile	Ile	His	Leu	Leu	Cys	Ile	Glu	
	770					775					780					
Pro	Met	Pro	His	Ser	Ala	Ile	Ala	Lys	Asn	Leu	Pro	Glu	Asn	Glu	Asn	
785					790					795					800	
Asn	Glu	Thr	Gly	Leu	Glu	Asn	Val	Ile	Asn	Lys	Val	Ala	Thr	Phe	Lys	
			805						810					815		

Lys Pro Gly Val Ser Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser
 820 825 830
 Leu Lys Asp Phe Asn Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His
 835 840 845
 Ser Lys Ala Glu His Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys
 850 855 860
 Asp Glu Ala Leu Pro Pro Pro Pro Pro Glu Phe Cys Pro Ala Phe
 865 870 875 880
 Ser Lys Val Ile Asn Leu Leu Asn Cys Asp Ile Met Met Tyr Ile Leu
 885 890 895
 Arg Thr Val Phe Glu Arg Ala Ile Asp Thr Asp Ser Asn Leu Trp Thr
 900 905 910
 Glu Gly Met Leu Gln Met Ala Phe His Ile Leu Ala Leu Gly Leu Leu
 915 920 925
 Glu Glu Lys Gln Gln Leu Gln Lys Ala Pro Glu Glu Glu Val Thr Phe
 930 935 940
 Asp Phe Tyr His Lys Ala Ser Arg Leu Gly Ser Ser Ala Met Asn Ile
 945 950 955 960
 Gln Met Leu Leu Glu Lys Leu Lys Gly Ile Pro Gln Leu Glu Gly Gln
 965 970 975
 Lys Asp Met Ile Thr Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg
 980 985 990
 Leu Arg Glu Lys Ser Cys Leu Ile Val Ala Thr Thr Ser Gly Ser Glu
 995 1000 1005
 Ser Ile Lys Asn Asp Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg
 1010 1015 1020
 Lys Arg Lys Ala Glu Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala
 1025 1030 1035 1040
 Gln Met Ser Ala Leu Gln Lys Asn Phe Ile Glu Thr His Lys Leu Met
 1045 1050 1055
 Tyr Asp Asn Thr Ser Glu Met Pro Gly Lys Glu Asp Ser Ile Met Glu
 1060 1065 1070
 Glu Glu Ser Thr Pro Ala Val Ser Asp Tyr Ser Arg Ile Ala Leu Gly
 1075 1080 1085
 Pro Lys Arg Gly Pro Ser Val Thr Glu Lys Glu Val Leu Thr Cys Ile
 1090 1095 1100
 Leu Cys Gln Glu Glu Gln Glu Val Lys Ile Glu Asn Asn Ala Met Val
 1105 1110 1115 1120
 Leu Ser Ala Cys Val Gln Lys Ser Thr Ala Leu Thr Gln His Arg Gly
 1125 1130 1135
 Lys Pro Ile Glu Leu Ser Gly Glu Ala Leu Asp Pro Leu Phe Met Asp
 1140 1145 1150

Pro Asp Leu Ala Tyr Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met
 1155 1160 1165
 His Ala Val Cys Trp Gln Lys Tyr Phe Glu Ala Val Gln Leu Ser Ser
 1170 1175 1180
 Gln Gln Arg Ile His Val Asp Leu Phe Asp Leu Glu Ser Gly Glu Tyr
 1185 1190 1195 1200
 Leu Cys Pro Leu Cys Lys Ser Leu Cys Asn Thr Val Ile Pro Ile Ile
 1205 1210 1215
 Pro Leu Gln Pro Gln Lys Ile Asn Ser Glu Asn Ala Asp Ala Leu Ala
 1220 1225 1230
 Gln Leu Leu Thr Leu Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile
 1235 1240 1245
 Ser Gly Tyr Asn Ile Arg His Ala Lys Gly Glu Asn Pro Ile Pro Ile
 1250 1255 1260
 Phe Phe Asn Gln Gly Met Gly Asp Ser Thr Leu Glu Phe His Ser Ile
 1265 1270 1275 1280
 Leu Ser Phe Gly Val Glu Ser Ser Ile Lys Tyr Ser Asn Ser Ile Lys
 1285 1290 1295
 Glu Met Val Ile Leu Phe Ala Thr Thr Ile Tyr Arg Ile Gly Leu Lys
 1300 1305 1310
 Val Pro Pro Asp Glu Arg Asp Pro Arg Val Pro Met Leu Thr Trp Ser
 1315 1320 1325
 Thr Cys Ala Phe Thr Ile Gln Ala Ile Glu Asn Leu Leu Gly Asp Glu
 1330 1335 1340
 Gly Lys Pro Leu Phe Gly Ala Leu Gln Asn Arg Gln His Asn Gly Leu
 1345 1350 1355 1360
 Lys Ala Leu Met Gln Phe Ala Val Ala Gln Arg Ile Thr Cys Pro Gln
 1365 1370 1375
 Val Leu Ile Gln Lys His Leu Val Arg Leu Leu Ser Val Val Leu Pro
 1380 1385 1390
 Asn Ile Lys Ser Glu Asp Thr Pro Cys Leu Leu Ser Ile Asp Leu Phe
 1395 1400 1405
 His Val Leu Val Gly Ala Val Leu Ala Phe Pro Ser Leu Tyr Trp Asp
 1410 1415 1420
 Asp Pro Val Asp Leu Gln Pro Ser Ser Val Ser Ser Ser Tyr Asn His
 1425 1430 1435 1440
 Leu Tyr Leu Phe His Leu Ile Thr Met Ala His Met Leu Gln Ile Leu
 1445 1450 1455
 Leu Thr Val Asp Thr Gly Leu Pro Leu Ala Gln Val Gln Glu Asp Ser
 1460 1465 1470
 Glu Glu Ala His Ser Ala Ser Ser Phe Phe Ala Glu Ile Ser Gln Tyr
 1475 1480 1485

Thr Ser Gly Ser Ile Gly Cys Asp Ile Pro Gly Trp Tyr Leu Trp Val
 1490 1495 1500
 Ser Leu Lys Asn Gly Ile Thr Pro Tyr Leu Arg Cys Ala Ala Leu Phe
 1505 1510 1515 1520
 Phe His Tyr Leu Leu Gly Val Thr Pro Pro Glu Glu Leu His Thr Asn
 1525 1530 1535
 Ser Ala Glu Gly Glu Tyr Ser Ala Leu Cys Ser Tyr Leu Ser Leu Pro
 1540 1545 1550
 Thr Asn Leu Phe Leu Leu Phe Gln Glu Tyr Trp Asp Thr Val Arg Pro
 1555 1560 1565
 Leu Leu Gln Arg Arg Cys Ala Asp Pro Ala Leu Leu Asn Cys Leu Lys
 1570 1575 1580
 Gln Lys Asn Thr Val Val Arg Tyr Pro Arg Lys Arg Asn Ser Leu Ile
 1585 1590 1595 1600
 Glu Leu Pro Asp Asp Tyr Ser Cys Leu Leu Asn Gln Ala Ser His Phe
 1605 1610 1615
 Arg Cys Pro Arg Ser Ala Asp Asp Glu Arg Lys His Pro Val Leu Cys
 1620 1625 1630
 Leu Phe Cys Gly Ala Ile Leu Cys Ser Gln Asn Ile Cys Cys Gln Glu
 1635 1640 1645
 Ile Val Asn Gly Glu Glu Val Gly Ala Cys Ile Phe His Ala Leu His
 1650 1655 1660
 Cys Lys Ala Arg Gly Cys Ala Tyr Pro Ala Pro Tyr Leu Asp Glu Tyr
 1665 1670 1675 1680
 Gly Glu Thr Asp Pro Gly Leu Lys Arg Gly Asn Pro Leu His Leu Ser
 1685 1690 1695
 Arg Glu Arg Tyr Arg Lys Leu His Leu Val Trp Gln Gln His Cys Ile
 1700 1705 1710
 Ile Glu Glu Ile Ala Arg Ser Gln Glu Thr Asn Gln Met Leu Phe Gly
 1715 1720 1725
 Phe Asn Trp Gln Leu Leu *
 1730 1735

<210> 20
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 20
 agaaggagag tacagtgcac tc

22

<210> 21
 <211> 20

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 21
 cgaaagcatc ctgtcctctg 20

 <210> 22
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 22
 aggaagctgt ggatcatgt 18

 <210> 23
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 23
 gtttaggaaga actg 14

 <210> 24
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 24
 aagaacagcg aaggcaacag 20

 <210> 25
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 25
 cgcagctacc ccaacacatt ct 22

 <210> 26
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 26
 tttcttccat tccctgcata ca 22

 <210> 27
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 27
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 <210> 28
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 28
 attccctgca tgcacttcag taa 23

 <210> 29
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

 <400> 29
 cattccctgc atgcattca g 21